

## SEQUENCE LISTING

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PFEFFERLE, WALTER

<120> NUCLEOTIDE SEQUENCE CODING FOR THE EXPORT OF  
BRANCHED CHAIN AMINO ACIDS, PROCESS FOR THE  
ISOLATION THEREOF AND USE THEREOF

<130> 7601/80525

<140>

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<150> US 09/471,803

<151> 1999-12-23

<150> DE 199 51 708.8

<151> 1999-10-27

<160> 12

<170> PatentIn Ver. 2.1

<210> 1

<211> 1271

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> gene

<222> (101)..(853)

<223> brnF

<220>

<221> gene

<222> (853)..(1176)

<223> brnE

<220>

<223> ATCC14752

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tcattcaagc	ctggagggtg	cgccatccaa	ggcagccctg	gaaccagatg	ataaagggtta	180
tcggcgctac	gaaatcgcg	aagggtctaaa	aacctccctt	gctgcagggt	tgggcatgta	240
cccgattggt	attgcgtttg	gtctcttggt	tattcaatac	ggctacgaat	ggtgggcagc	300
cccactgttt	tccggcctga	ttttcgcggg	ctccaccgaa	atgctggtca	tcgccctcgt	360
tgtgggcgca	gcgcccctgg	gcgccatcgc	gctcaccaca	ttgctggtga	acttccgcca	420
cgtattctat	gcgttttcat	tcccgttgca	tgtggtcaaa	aaccccatg	cccgtttcta	480
ttcggttttc	gcgcttatcg	acgaagccta	cgcagtcact	gcggccaggc	ccgcaggctg	540
gtcggcgtgg	cgacttatct	caatgcaaat	agcgtttcac	tcctactggg	tattcggcgg	600
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cctttgtctt	ctctttgtca	cgctgacttt	ggattcctgc	cgaacgaaaa	agcagatccc	720
ttctctgctg	ctcgcagggt	tgagcttcac	cattgctctt	gtggtaatc	caggtcaggc	780
cctatttgcg	gcgctgtgta	tcttcttggt	tctgttgacc	atccggtact	tcttcttggt	840
aaaggctgct	aaatgacaac	tgattttctc	tgtattctcc	ttgttgctgc	agtatgtgca	900
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caatttggtg	gcaaaatggc	gatgtggatg	ccagcaggaa	tccttgccat	tttgaccgca	1020
tcaacgtttc	gcagcaatgc	gatagatctg	aagactctaa	cctttggtct	cattgccgtt	1080
gcgattacag	tggtggcgca	tcttcttggt	ggtcgacgca	ccttggtgag	cgttggcgct	1140

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ggcaccatcg tttttgttgg actggtgaat cttttctaaa actgcataaa taacaaaaaat 1200
ccgcatgccc tcaatttgaa ggggatgcgg attttttaag gaacctagaa aaggcttaag 1260
cagacagcgc t                                     1271

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<210> 2
<211> 753
<212> DNA
<213> Corynebacterium glutamicum

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<220>
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<222> (1)..(753)
<223> brnF

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<220>
<223> ATCC14752

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<400> 2
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1 5 10 15

aag gca gcc ctg gaa cca gat gat aaa ggt tat cgg cgc tac gaa atc 96
Lys Ala Ala Leu Glu Pro Asp Asp Lys Gly Tyr Arg Arg Tyr Glu Ile
20 25 30

gcg caa ggt cta aaa acc tcc ctt gct gca ggt ttg ggc atg tac ccg 144
Ala Gln Gly Leu Lys Thr Ser Leu Ala Ala Gly Leu Gly Met Tyr Pro
35 40 45

att ggt att gcg ttt ggt ctc ttg gtt att caa tac ggc tac gaa tgg 192
Ile Gly Ile Ala Phe Gly Leu Leu Val Ile Gln Tyr Gly Tyr Glu Trp
50 55 60

tgg gca gcc cca ctg ttt tcc ggc ctg att ttc gcg ggc tcc acc gaa 240
Trp Ala Ala Pro Leu Phe Ser Gly Leu Ile Phe Ala Gly Ser Thr Glu
65 70 75 80

atg ctg gtc atc gcc ctc gtt gtg ggc gca gcg ccc ctg ggc gcc atc 288
Met Leu Val Ile Ala Leu Val Val Gly Ala Ala Pro Leu Gly Ala Ile
85 90 95

gcg ctc acc aca ttg ctg gtg aac ttc cgc cac gta ttc tat gcg ttt 336
Ala Leu Thr Thr Leu Leu Val Asn Phe Arg His Val Phe Tyr Ala Phe
100 105 110

tca ttc ccg ctg cat gtg gtc aaa aac ccc att gcc cgt ttc tat tcg 384
Ser Phe Pro Leu His Val Val Lys Asn Pro Ile Ala Arg Phe Tyr Ser
115 120 125

gtt ttc gcg ctt atc gac gaa gcc tac gca gtc act gcg gcc agg ccc 432
Val Phe Ala Leu Ile Asp Glu Ala Tyr Ala Val Thr Ala Ala Arg Pro
130 135 140

gca ggc tgg tcg gcg tgg cga ctt atc tca atg caa ata gcg ttt cac 480
Ala Gly Trp Ser Ala Trp Arg Leu Ile Ser Met Gln Ile Ala Phe His
145 150 155 160

tcc tac tgg gta ttc ggc ggt ctc acc gga gtg gcg atc gca gag ttg 528
Ser Tyr Trp Val Phe Gly Gly Leu Thr Gly Val Ala Ile Ala Glu Leu
165 170 175

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att cct ttt gaa att aag ggc ctc gag ttc gcc ctt tgc tct ctc ttt 576
Ile Pro Phe Glu Ile Lys Gly Leu Glu Phe Ala Leu Cys Ser Leu Phe
180 185 190

gtc acg ctg act ttg gat tcc tgc cga acg aaa aag cag atc cct tct 624
Val Thr Leu Thr Leu Asp Ser Cys Arg Thr Lys Lys Gln Ile Pro Ser
195 200 205

ctg ctg ctc gca ggt ttg agc ttc acc att gct ctt gtg gta att cca 672
Leu Leu Leu Ala Gly Leu Ser Phe Thr Ile Ala Leu Val Val Ile Pro
210 215 220

ggg cag gcc cta ttt gcg gcg ctg ctg atc ttc ttg ggt ctg ttg acc 720
Gly Gln Ala Leu Phe Ala Ala Leu Leu Ile Phe Leu Gly Leu Leu Thr
225 230 235 240

atc cgg tac ttc ttc ttg gga aag gct gct aaa 753
Ile Arg Tyr Phe Phe Leu Gly Lys Ala Ala Lys
245 250

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<210> 3
<211> 251
<212> PRT
<213> Corynebacterium glutamicum

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<220>
<223> ATCC14752

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<400> 3
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1 5 10 15

Lys Ala Ala Leu Glu Pro Asp Asp Lys Gly Tyr Arg Arg Tyr Glu Ile
20 25 30

Ala Gln Gly Leu Lys Thr Ser Leu Ala Ala Gly Leu Gly Met Tyr Pro
35 40 45

Ile Gly Ile Ala Phe Gly Leu Leu Val Ile Gln Tyr Gly Tyr Glu Trp
50 55 60

Trp Ala Ala Pro Leu Phe Ser Gly Leu Ile Phe Ala Gly Ser Thr Glu
65 70 75 80

Met Leu Val Ile Ala Leu Val Val Gly Ala Ala Pro Leu Gly Ala Ile
85 90 95

Ala Leu Thr Thr Leu Leu Val Asn Phe Arg His Val Phe Tyr Ala Phe
100 105 110

Ser Phe Pro Leu His Val Val Lys Asn Pro Ile Ala Arg Phe Tyr Ser
115 120 125

Val Phe Ala Leu Ile Asp Glu Ala Tyr Ala Val Thr Ala Ala Arg Pro
130 135 140

Ala Gly Trp Ser Ala Trp Arg Leu Ile Ser Met Gln Ile Ala Phe His
145 150 155 160

Ser Tyr Trp Val Phe Gly Gly Leu Thr Gly Val Ala Ile Ala Glu Leu
165 170 175

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Ile Pro Phe Glu Ile Lys Gly Leu Glu Phe Ala Leu Cys Ser Leu Phe  
180 185 190

Val Thr Leu Thr Leu Asp Ser Cys Arg Thr Lys Lys Gln Ile Pro Ser  
195 200 205

Leu Leu Leu Ala Gly Leu Ser Phe Thr Ile Ala Leu Val Val Ile Pro  
210 215 220

Gly Gln Ala Leu Phe Ala Ala Leu Leu Ile Phe Leu Gly Leu Leu Thr  
225 230 235 240

Ile Arg Tyr Phe Phe Leu Gly Lys Ala Ala Lys  
245 250

<210> 4  
<211> 324  
<212> DNA  
<213> *Corynebacterium glutamicum*

<220>  
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<222> (1)..(324)  
<223> brnE

<220>  
<223> ATCC14752

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gtc att act ttt gcg ctc cgg gcg gtt ccg ttc tta atc ctt aag ccc 96  
Val Ile Thr Phe Ala Leu Arg Ala Val Pro Phe Leu Ile Leu Lys Pro  
20 25 30

cta cgt gaa tca caa ttt gtg ggc aaa atg gcg atg tgg atg cca gca 144  
Leu Arg Glu Ser Gln Phe Val Gly Lys Met Ala Met Trp Met Pro Ala  
35 40 45

gga atc ctt gcc att ttg acc gca tca acg ttt cgc agc aat gcg ata 192  
Gly Ile Leu Ala Ile Leu Thr Ala Ser Thr Phe Arg Ser Asn Ala Ile  
50 55 60

gat ctg aag act cta acc ttt ggt ctc att gcc gtt gcg att aca gtg 240  
Asp Leu Lys Thr Leu Thr Phe Gly Leu Ile Ala Val Ala Ile Thr Val  
65 70 75 80

gtg gcg cat ctt ctt ggc ggt cga cgc acc ttg ttg agc gtt ggc gct 288  
Val Ala His Leu Leu Gly Gly Arg Arg Thr Leu Leu Ser Val Gly Ala  
85 90 95

ggc acc atc gtt ttt gtt gga ctg gtg aat ctt ttc 324  
Gly Thr Ile Val Phe Val Gly Leu Val Asn Leu Phe  
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<210> 5  
<211> 108  
<212> PRT

<213> *Corynebacterium glutamicum*

<220>

<223> ATCC14752

<400> 5

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Val Ile Thr Phe Ala Leu Arg Ala Val Pro Phe Leu Ile Leu Lys Pro
          20          25          30

Leu Arg Glu Ser Gln Phe Val Gly Lys Met Ala Met Trp Met Pro Ala
          35          40          45

Gly Ile Leu Ala Ile Leu Thr Ala Ser Thr Phe Arg Ser Asn Ala Ile
          50          55          60

Asp Leu Lys Thr Leu Thr Phe Gly Leu Ile Ala Val Ala Ile Thr Val
          65          70          75          80

Val Ala His Leu Leu Gly Gly Arg Arg Thr Leu Leu Ser Val Gly Ala
          85          90          95

Gly Thr Ile Val Phe Val Gly Leu Val Asn Leu Phe
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<210> 6

<211> 1271

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> gene

<222> (101)..(853)

<223> brnF

<220>

<221> gene

<222> (853)..(1176)

<223> brnE

<220>

<223> ATCC13032

<400> 6

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tcattcaagc ctggagggtg cgccatccaa ggcagccctg gaaccagatg ataaaggtta 180
tcggcgctac gaaatcgcg aaggtctaaa aacctccctt gctgcagggt tgggcatgta 240
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tgtgggcgca gcgcccctgg gcgccatcgc gctcaccaca ttgctggtga acttcgcca 420
cgtattctat gcgttttcat tcccgctgca tgtgggtcaaa aaccccatg cccgtttcta 480
ttcggttttc gcgttatcgc acgaagccta cgcagtcact gcggccaggc ccgcaggctg 540
gtcggcggtg cgacttatct caatgcaaat agcgtttcac tcctactggg tattcggcgg 600
tctcaccgga gtggcgatcg cagagttgat tccttttgaa attaagggcc tcgagttcgc 660
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ttctctgctg ctgcgagggt tgagcttcac cattgctctt gtggtaattc caggtcaggc 780
cctatttgcg gcgctgctga tcttcttggg tctgttgacc atccggtact tcttcttggg 840
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gtcattacttt ttgcgctccg ggcgggttccg ttcttaatcc ttaagcccct acgtgaatca 960
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tcaacgtttc gcagcaatgc gatagatctg aagactctaa cctttggtct cattgccgtt 1080
gcgattacag tgggtggcgca tcttcttggc ggtcgacgca ccttggtgag cgttggcgct 1140
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<210> 7
<211> 24
<212> DNA
<213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence: Primer

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<400> 7
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<210> 8
<211> 24
<212> DNA
<213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence: Primer

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<400> 8
gcgcgatcaa tggaatctag cttc                                     24

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<210> 9
<211> 17
<212> DNA
<213> Artificial sequence

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<220>
<223> Description of artificial sequence: Universal
      Primer

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<400> 9
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```

```

<210> 10
<211> 19
<212> DNA
<213> Artificial sequence

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<220>
<223> Description of artificial sequence: Reverse
      Primer

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<400> 10
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<210> 11
<211> 23
<212> DNA
<213> Artificial Sequence

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<220>

<223> Description of Artificial Sequence: Primer

<400> 11

cggtctaca ccgctagccc agg

23

<210> 12

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 12

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20